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# Allozyme Genotypes for Popular and Historically Important Inbred Lines of Corn, *Zea mays* L.

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# Allozyme Genotypes for Popular and Historically Important Inbred Lines of Corn, *Zea mays* L.

By C. W. Stuber<sup>1</sup> and M. M. Goodman<sup>2</sup>

## ABSTRACT

Allozymes (enzyme variants) determined by electrophoresis and ascribed to 23 genetic loci were studied in a survey of more than 400 inbred lines of corn, *Zea mays* L. Most of the lines surveyed were from the United States and Canada with a few from Europe, Latin America, and India. For the 23 loci evaluated, 80 alleles were detected in 406 lines of corn. This is 80/245 (33%) of the alleles that have been ascertained in corn and teosinte. In a subset of 39 of the most widely used publicly available lines, 51 alleles were detected. There were 36 (92%) distinct allozyme genotypes found in this set of widely used lines; 33 (85%) of the 39 lines were unique within the set. Subsets of white corn, sweet corn, and popcorn lines were also evaluated and summarized. Index terms: allozymes, corn, corn lines, enzymes, isozymes, plant genetics, teosinte, *Zea mays* L.

## INTRODUCTION

A significant aspect of our current research has been the elucidation of the basic genetics of isozyme variants (determined by electrophoresis) in corn (*Zea mays* L.) and teosinte (*Zea* spp.). This research has included numerous allelism tests, linkage studies, and gene-localization studies. Much of the work on basic genetics has evolved because of a second aspect of our current research, a survey of the isozyme variants in the races (about 250) of corn, most of them from Latin American countries. We have also surveyed nearly all the available populations of teosinte. As each new region or country is surveyed, new isozyme var-

iants are encountered. We routinely subject these variants to allelism tests to ascertain proper locus assignment and regularity of genetic segregation.

These new isozyme variants frequently occur in populations that are difficult to grow in the corn-producing areas of the United States, particularly during the summer, and sources of these variants in more easily grown types of corn were desired. Therefore, it was decided to survey a large group of popular, historic, and widely divergent inbred lines of corn to: (1) identify sources of rare alleles at enzyme loci in cultivars or lines that are more easily handled and more readily replicated than individual plants (or their selfed progeny) of the many exotic races being studied, and (2) characterize the germplasm in use in the United States so that it could be compared with germplasm of the Latin American races. Although most of the inbred lines surveyed are from the United States, several lines from Canada and a few from Europe, Latin America, and India were also assayed. A similar survey was done in Canada by Cardy

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(1981); Cardy and Kannenberg (1982); and Cardy, Kannenberg, and Dhesi (1980) involving primarily Canadian inbred lines and hybrids of corn. The results of these surveys should be useful not only for genotypic identification, or "fingerprinting," of lines and hybrids but also as a means for establishing cultivar identity or uniqueness.

A shorter version of the following report appeared in Goodman and Stuber (1980). This expanded version includes our complete survey of allozymes for 421 publicly available inbred lines of corn, 406 from the United States, Canada, and Europe and 15 from Latin America and India. In the list of 406 lines, only 391 differently named lines exist, but, for reasons explained later, we listed 15 lines twice. When possible, we obtained seeds for each line from the experiment station where it originated.

## ELECTROPHORETIC ASSAYS

Electrophoretic techniques used were essentially the same as those reported by Cardy, Stuber, and Goodman (1980); Goodman, Stuber, Lee, and Johnson (1980); and Stuber et al. (1977, 1980). These procedures are briefly reviewed below. For analyses, we used coleoptilar sections, 1.2 cm long, from 5-day-old seedlings grown in darkness at 22° C. Each section was homogenized in a solution containing 16.7% sucrose and 8.3% sodium ascorbate (pH 7.38) in a 400- $\mu$ l polyethylene microcentrifuge tube using a power-driven acetal pestle. The homogenate was centrifuged for 4 minutes in a refrigerated microcentrifuge and then stored at -60° C or lower for later electrophoretic analyses. Filter-paper wicks (2 by 11 mm) were used to absorb samples of thawed supernatant for insertion into a slit in a starch gel.

The gels (13% starch) were prepared by suspending starch in a suitable buffer solution, heating the mixture until a clear, vigorously boiling solution was obtained, degassing with an aspirator, and pouring into an acrylic mold. Gels were cooled, covered with plastic film, and left at room temperature overnight. Usually, 28 plant samples (4 controls having known banding patterns and 24 experimentals) were placed in each gel for electrophoresis.

We used four different buffer systems:

A. L-Histidine and citric acid, pH 5.0.

B. L-Histidine and citric acid, pH 5.7.

C. Tris-citrate and lithium hydroxide-boric acid, pH 8.3.

D. L-Histidine and citric acid, pH 6.5.

Although resolution of some enzyme banding patterns was possible with a single buffer system, several required two systems. Most enzymes required about 1 hour of incubation of the gel in the staining solution; a few were left overnight. Procedures and specific staining techniques used for each enzyme were as follows (buffer systems are referred to as A, B, C, or D as noted above):

*Acid phosphatase (ACP).*—Both the B and D buffer systems were used for resolution of ACP. Zones of enzyme activity were revealed with a solution of 50 ml 0.1 M sodium acetate-acetic acid buffer (pH 5.0), 200 mg Diazo Blue B (o-dianisidine, tetrazotized) and 200 mg  $\alpha$ -naphthyl acid phosphate.

*Alcohol dehydrogenase (ADH).*—C buffer system was used for electrophoresis. ADH activity was detected using 25 ml 0.1 M tris-HCl buffer (pH 8.5), 0.5 ml ethanol, 10 mg  $\beta$ -nicotinamide adenine dinucleotide, 10 mg nitro blue tetrazolium, and 2.5 mg phenazine methosulfate.

*Catalase (CAT).*—Both C and D buffer systems were used for resolution of CAT banding patterns. The staining procedure used 0.01% H<sub>2</sub>O<sub>2</sub>, which was poured on the gel slice for 7–10 minutes. This was rinsed with distilled water, and the gel was then immersed in a solution of 50 ml H<sub>2</sub>O, 500 mg potassium ferricyanide, and 500 mg ferric chloride.

*Endopeptidase (ENP).*—C buffer system was used for electrophoresis. ENP activity was revealed using 50 ml of a tris-maleic acid-NaOH buffer (pH 5.55), 25 mg  $\alpha$ -N-benzoyl-DL-arginine- $\beta$ -naphthylamide HCl, 25 mg Black K salt, and 50 mg MgCl<sub>2</sub>.

*Esterase (EST).*—C buffer system was used for electrophoresis of EST. The staining solution was 50 ml sodium phosphate buffer (pH 6.0), 2.5 ml N-propanol, 20 mg  $\beta$ -naphthyl acetate, and 25 mg Fast Garnet GBC salt.

*$\beta$ -Glucosidase ( $\beta$ -GLU).*—Electrophoresis used the B buffer system. Zones of enzyme activity were revealed with 50 mg 6-bromo-2-naphthyl- $\beta$ -D-glucoside dissolved in 5 ml acetone, 70 ml 0.05 M potassium phosphate buffer (pH 6.5), 1.2 g polyvinylpyrrolidone (PVP-40), and 100 mg Fast Blue BB salt.

*Glutamate-oxaloacetate transaminase (GOT).*—C buffer system was used for electrophoresis. GOT



activity was detected with 50 mg Fast Blue BB salt in 25 ml H<sub>2</sub>O mixed with a solution of 18.3 mg  $\alpha$ -ketoglutaric acid, 66.6 mg L-aspartic acid, 250 mg polyvinylpyrrolidone (PVP-40), 25 mg ethylenediamine tetra-acetic acid disodium salt, 710 mg Na<sub>2</sub>HPO<sub>4</sub>, and 25 ml H<sub>2</sub>O.

*Isocitrate dehydrogenase (IDH).*—Electrophoresis used the D buffer system. The staining procedure involved an agar overlay; 15 ml 0.1 M tris-HCl buffer (pH 9.1) was added to 150 mg DL-isocitric acid, 15 mg nicotinamide adenine dinucleotide phosphate, 10 mg nitro blue tetrazolium, and 0.5 mg phenazine methosulfate. That solution was mixed with a cooled (72° C) agar solution consisting of 200 mg agar, 300 mg polyvinylpyrrolidone (PVP-40), and 15 ml 0.1 M tris-HCl buffer (pH 9.1).

*Malate dehydrogenase (MDH).*—Both the A and B buffer systems were used for electrophoresis. Zones of enzyme activity were revealed with 50 ml 0.1 M tris-HCl buffer (pH 9.1), 100 mg malic acid (neutralized with NaOH to pH 9.0), 20 mg  $\beta$ -nicotinamide adenine dinucleotide, 10 mg nitro blue tetrazolium, and 1.25 mg phenazine methosulfate.

*Malic enzyme (ME).*—Electrophoresis used the B buffer system. The staining solution was 50 ml

0.1 M tris-HCl buffer (pH 8.5), 25 mg DL-malic acid (neutralized with NaOH to pH 9.0), 50 mg MgCl<sub>2</sub>, 13 mg nicotinamide adenine dinucleotide phosphate, 10 mg nitro blue tetrazolium, and 1 mg phenazine methosulfate.

*Phosphoglucumutase (PGM).*—The A and D buffer systems were required for resolution of PGM bands. PGM activity was detected using 50 ml 0.1 M tris-HCl buffer (pH 8.5), 250 mg  $\alpha$ -D-glucose-1-phosphate disodium salt, 25 mg ethylenediamine tetra-acetic acid disodium salt, 100 mg MgCl<sub>2</sub>, 5 mg nicotinamide adenine dinucleotide phosphate, 7.5 mg tetrazolium thiazolyl blue, 1 mg phenazine methosulfate, and 37.5 units glucose-6-phosphate dehydrogenase.

*6-Phosphogluconate dehydrogenase (6-PGD).* Both the B and D buffer systems were used. The staining solution was 50 ml 0.05 M tris-HCl buffer (pH 8.0), 20 mg 6-phosphogluconic acid trisodium salt, 50 mg MgCl<sub>2</sub>, 5 mg nicotinamide adenine dinucleotide phosphate, 6 mg tetrazolium thiazolyl blue, and 1.5 mg phenazine methosulfate.

*Phosphohexose isomerase (PHI).*—As for 6-PGD, both B and D buffer systems were used for electrophoresis. Zones of enzyme activity were revealed with a solution of 50 ml 0.05 M tris-

Table 1.—Enzyme loci and their chromosomal locations in corn

Locus	Enzyme	Chromosomal location
<i>Acp1</i> .....	Acid phosphatase-1 .....	9
<i>Adh1</i> .....	Alcohol dehydrogenase-1 .....	1L
<i>Cat3</i> .....	Catalase-3 .....	Unknown
<i>E8</i> .....	Esterase-8 .....	3S
<i>Enp1</i> .....	Endopeptidase .....	6L
<i>Glu1</i> .....	$\beta$ -Glucosidase .....	10L
<i>Got1</i> .....	Glutamate-oxaloacetate transaminase-1 .....	3L
<i>Got2</i> .....	Glutamate-oxaloacetate transaminase-2 .....	5L
<i>Got3</i> .....	Glutamate-oxaloacetate transaminase-3 .....	5S
<i>Idh1</i> .....	Isocitrate dehydrogenase-1 .....	8
<i>Idh2</i> .....	Isocitrate dehydrogenase-2 .....	6L
<i>Mdh1</i> .....	Malate dehydrogenase-1 .....	8
<i>Mdh2</i> .....	Malate dehydrogenase-2 .....	6L
<i>Mdh3</i> .....	Malate dehydrogenase-3 .....	3L
<i>Mdh4</i> .....	Malate dehydrogenase-4 .....	1L
<i>Mdh5</i> .....	Malate dehydrogenase-5 .....	5S
<i>Me1</i> .....	Malic enzyme .....	3L
<i>Mmm</i> .....	Modifier of mitochondrial MDH's .....	1L
<i>Pgd1</i> .....	6-Phosphogluconate dehydrogenase-1 .....	6L
<i>Pgd2</i> .....	6-Phosphogluconate dehydrogenase-2 .....	3L
<i>Pgm1</i> .....	Phosphoglucumutase-1 .....	1L
<i>Pgm2</i> .....	Phosphoglucumutase-2 .....	5S
<i>Phi1</i> .....	Phosphohexose isomerase .....	1L

Table 2.—Intralocus and interlocus hybrid banding patterns for each of the enzyme systems assayed in corn

Enzyme	Hybrid banding pattern		
	None	Intralocus only	Both intralocus and interlocus
Single-locus: <sup>1</sup>			
ENP .....	X	.....	.....
ACP .....		X	.....
ADH .....		X	.....
CAT .....		X	.....
EST .....		X	.....
$\alpha$ -GLU .....		X	.....
ME .....		X	.....
PHI .....		X	.....
Multiple-locus:			
PGM ....	X	.....	.....
GOT .....		X	.....
IDH .....			X
MDH .....			X
6-PGD .....			X

<sup>1</sup>In tissues other than coleoptiles and with other assay techniques, some of these enzymes (ACP, ADH, CAT, EST, ME, PHI) can be shown to have additional bands governed by additional loci.

HCl buffer (pH 8.0), 50 mg D-fructose-6-phosphate, 50 mg MgCl<sub>2</sub>, 5 mg nicotinamide adenine dinucleotide phosphate, 5 mg tetrazolium thiazolyl blue, 1.5 mg phenazine methosulfate, and 10 units glucose-6-phosphate dehydrogenase. Adding 20 mg of 6-phosphogluconic acid trisodium salt allows both PHI and 6-PGD to be stained on the same gel slice.

## GENETIC ANALYSES OF ISOZYME BANDS IN CORN AND TEOSINTE

The isozyme variants in about 1,600 corn lines, populations, and collections that we have studied so far have been ascribed to 23 genetic loci distributed among all of the corn chromosomes except chromosomes 2, 4, and 7. Chromosomal locations and linkage relationships among those loci located on the same chromosomes have been reported by Goodman, Stuber, Newton, and Weissinger (1980). Table 1 summarizes the loci and their chromosomal locations.

Studies of isozyme variants in about 40 populations of teosinte, a very close relative of corn, have been reported by Doebley et al. (1983) and

Smith et al. (1983). Although it appears that corn and teosinte share the same loci, some of the specific isozyme variants found in teosinte have not yet been identified in corn.

We have found that, for those enzyme systems encoded by a single locus, the association of isozyme bands with specific alleles is generally easily established. Usually, one band can be ascribed to each allele; for most systems there is an additional "hybrid" band that usually falls midway between the allelic isozyme bands. (Occasionally, more than one hybrid band is present.) These are referred to as intralocus hybrid bands. For multiple-locus enzymes, the banding patterns are more complex, and it is usually much more difficult to establish direct association between banding patterns and specific alleles at the various loci. Frequently, the bands from different loci overlap on the gels, and most systems form intralocus hybrid bands or both intralocus and interlocus hybrid bands. A classification of the enzyme systems according to number of loci and hybrid banding patterns is shown in table 2.

In multilocus enzyme systems, a few of the bands associated with one locus comigrate with bands from a second locus and cannot be scored with a single electrophoretic buffer system. Most of these scoring problems caused by comigration can be resolved by assaying the samples with two buffer systems. But the scoring of two frequently occurring MDH bands presents problems even when two buffer systems are used. The band associated with the allele designated *Mdh1-6* stains lightly and comigrates with the band associated with allele *Mdh2-6*, which stains darkly. When the *Mdh2-6* band is present and no *Mdh1* band is visible, the scoring for the *Mdh1* locus can be either *Mdh1-6* or *Mdh1-n* (*n* symbolizes a recessive null allele). Because the *Mdh1-n* allele is rarely found, we have assumed that the *Mdh1-6* allele is present whenever this situation occurs. We have made a similar assumption for the *Mdh5-12* band, which comigrates with and is masked by *Mdh4-12*.

All of the loci studied are polymorphic with a range of 3 alleles detected for *Mmm* to 31 alleles detected for *Glu1*. We have detected and verified 245 alleles in our studies (table 3). Although most of these alleles have been found in corn, about 14% (34) have been found only in teosinte. Many alleles originally found only in teosinte have subsequently been found in corn as we have

(Continued on page 8.)

Table 3.—Number of alleles detected at each locus in 406 U.S., Canadian, and European inbred lines of corn and in all corn and teosinte surveyed

Locus	406 Inbred lines					All corn and teosinte surveyed <sup>1</sup>			
	Entire set	Widely used <sup>2</sup> (39 lines)	White corn (45 lines)	Sweet corn (39 lines)	Pop-corn (22 lines)	Teosinte and corn	Teosinte only	Corn only	Total
<i>Acp1</i> . . . . .	6	4	4	4	4	9	2	2	13
<i>Adh1</i> . . . . .	3	2	2	3	2	3	1	2	6
<i>Cat3</i> . . . . .	4	2	3	3	3	4	1	3	8
<i>E8</i> . . . . .	5	3	4	4	2	8	0	1	9
<i>Enp1</i> . . . . .	6	2	5	4	2	5	2	2	9
<i>Glu1</i> . . . . .	9	6	4	5	3	24	2	5	31
<i>Got1</i> . . . . .	2	2	2	1	2	4	2	3	9
<i>Got2</i> . . . . .	2	2	2	2	1	5	0	3	8
<i>Got3</i> . . . . .	1	1	1	1	1	5	0	1	6
<i>Idh1</i> . . . . .	3	2	2	1	1	3	0	2	5
<i>Idh2</i> . . . . .	3	2	2	2	2	4	1	3	8
<i>Mdh1</i> . . . . .	4	2	4	3	1	5	3	8	16
<i>Mdh2</i> . . . . .	6	3	4	2	3	7	6	8	21
<i>Mdh3</i> . . . . .	2	2	2	1	1	4	2	2	8
<i>Mdh4</i> . . . . .	2	1	1	1	1	3	2	6	11
<i>Mdh5</i> . . . . .	4	2	2	2	1	5	0	7	12
<i>Me1</i> . . . . .	1	1	1	1	1	1	1	2	4
<i>Mmm</i> . . . . .	2	1	2	2	1	2	0	1	3
<i>Pgd1</i> . . . . .	3	3	3	2	2	7	2	0	9
<i>Pgd2</i> . . . . .	2	2	1	1	1	3	0	2	5
<i>Pgm1</i> . . . . .	2	1	2	2	1	9	3	5	17
<i>Pgm2</i> . . . . .	4	3	3	3	2	8	4	6	18
<i>Phi1</i> . . . . .	4	2	3	1	1	8	0	1	9
Total . . . . .	80	51	59	51	39	136	34	75	245

<sup>1</sup>About 1,600 lines, populations, and collections including those in this survey.

<sup>2</sup>The publicly available lines most widely used as parents for hybrids planted in 1980 (Zuber and Darrah 1980). Each line was used as a parent for more than 1 million pounds of hybrid seed.

Table 4.—Alleles detected and their frequencies in the entire set and 4 subsets of 406 U.S., Canadian, and European inbred lines of corn

Locus and allele <sup>1</sup>	Allele frequency				
	Entire set	Widely used <sup>2</sup>	White corn	Sweet corn	Popcorn
<i>Acp1</i> :					
<i>Acp1-2</i> . . . . .	0.323	0.33	0.36	0.10	0.64
<i>Acp1-2L</i> . . . . .	.002	.00	.00	.00	.04
<i>Acp1-2*</i> . . . . .	.010	.00	.02	.03	.00
<i>Acp1-3</i> . . . . .	.123	.08	.27	.05	.09
<i>Acp1-4</i> . . . . .	.527	.56	.36	.82	.23
<i>Acp1-6</i> . . . . .	.015	.03	.00	.00	.00

See footnotes at end of table.



Table 4.—Alleles detected and their frequencies in the entire set and 4 subsets of 406 U.S., Canadian, and European inbred lines of corn—Continued

Locus and allele <sup>1</sup>	Allele frequency				
	Entire set	Widely used <sup>2</sup>	White corn	Sweet corn	Popcorn
<i>Adh1:</i>					
<i>Adh1-4</i> .....	0.862	0.97	0.87	0.54	0.95
<i>Adh1-6</i> .....	.133	.03	.13	.44	.05
<i>Adh1-n</i> .....	.005	.00	.00	.03	.00
<i>Cat3:</i>					
<i>Cat3-7</i> .....	.005	.00	.00	.00	.00
<i>Cat3-9</i> .....	.879	.92	.87	.69	.68
<i>Cat3-12</i> .....	.084	.08	.11	.18	.05
<i>Cat3-n</i> .....	.032	.00	.02	.13	.27
<i>E8:</i>					
<i>E8-4</i> .....	.323	.21	.24	.74	.64
<i>E8-4.5</i> .....	.367	.36	.44	.15	.36
<i>E8-5</i> .....	.293	.44	.27	.00	.00
<i>E8-6</i> .....	.012	.00	.04	.05	.00
<i>E8-n</i> .....	.005	.00	.00	.05	.00
<i>Enp1:</i>					
<i>Enp1-4</i> .....	.015	.03	.13	.00	.00
<i>Enp1-6</i> .....	.931	.97	.71	.85	.73
<i>Enp1-8</i> .....	.022	.00	.07	.00	.27
<i>Enp1-10</i> .....	.020	.00	.04	.08	.00
<i>Enp1-12</i> .....	.002	.00	.00	.03	.00
<i>Enp1-n</i> .....	.010	.00	.04	.05	.00
<i>Glu1:</i>					
<i>Glu1-1</i> .....	.059	.03	.04	.08	.00
<i>Glu1-2</i> .....	.131	.08	.20	.10	.00
<i>Glu1-2.5</i> .....	.002	.00	.00	.03	.00
<i>Glu1-3</i> .....	.017	.05	.00	.00	.00
<i>Glu1-6</i> .....	.264	.28	.16	.08	.09
<i>Glu1-7</i> .....	.473	.54	.60	.72	.86
<i>Glu1-9</i> .....	.002	.00	.00	.00	.00
<i>Glu1-10</i> .....	.015	.00	.00	.00	.00
<i>Glu1-n</i> .....	.037	.03	.00	.00	.05
<i>Got1:</i>					
<i>Got1-4</i> .....	.916	.92	.91	1.00	.73
<i>Got1-6</i> .....	.084	.08	.09	.00	.27
<i>Got2:</i>					
<i>Got2-2</i> .....	.084	.10	.04	.18	.00
<i>Got2-4</i> .....	.916	.90	.96	.82	1.00
<i>Got3, Got3-4</i> .....	1.00	1.00	1.00	1.00	1.00
<i>Idh1:</i>					
<i>Idh1-4</i> .....	.968	.97	.96	1.00	1.00
<i>Idh1-6</i> .....	.030	.00	.04	.00	.00
<i>Idh1-8</i> .....	.002	.03	.00	.00	.00
<i>Idh2:</i>					
<i>Idh2-4</i> .....	.480	.23	.49	.26	.86
<i>Idh2-4.2</i> .....	.002	.00	.00	.00	.00
<i>Idh2-6</i> .....	.517	.77	.51	.74	.14
<i>Mdh1:</i>					
<i>Mdh1-1</i> .....	.096	.08	.29	.03	.00
<i>Mdh1-6</i> .....	.860	.92	.64	.64	1.00
<i>Mdh1-10.5</i> .....	.039	.00	.02	.33	.00
<i>Mdh1-n</i> .....	.005	.00	.04	.00	.00

See footnotes at end of table.

Table 4.—Alleles detected and their frequencies in the entire set and 4 subsets of 406 U.S., Canadian, and European inbred lines of corn—Continued

Locus and allele <sup>1</sup>	Allele frequency				
	Entire set	Widely used <sup>2</sup>	White corn	Sweet corn	Popcorn
<i>Mdh2:</i>					
<i>Mdh2-3</i> .....	0.261	0.23	0.47	0.03	0.09
<i>Mdh2-3.5</i> .....	.227	.10	.16	.00	.41
<i>Mdh2-4.5</i> .....	.007	.00	.00	.00	.00
<i>Mdh2-5.6</i> .....	.002	.00	.00	.00	.00
<i>Mdh2-6</i> .....	.495	.67	.31	.97	.50
<i>Mdh2-n</i> .....	.007	.00	.07	.00	.00
<i>Mdh3:</i>					
<i>Mdh3-16</i> .....	.914	.97	.96	1.00	1.00
<i>Mdh3-18</i> .....	.086	.03	.04	.00	.00
<i>Mdh4:</i>					
<i>Mdh4-12</i> .....	.995	1.00	1.00	1.00	1.00
<i>Mdh4-14.5</i> .....	.005	.00	.00	.00	.00
<i>Mdh5:</i>					
<i>Mdh5-12</i> .....	.975	.97	.98	.95	1.00
<i>Mdh5-15</i> .....	.015	.00	.00	.05	.00
<i>Mdh5-16.4</i> .....	.002	.00	.00	.00	.00
<i>Mdh5-n</i> .....	.007	.03	.02	.00	.00
<i>Me1, Me1-R</i> .....	1.00	1.00	1.00	1.00	1.00
<i>Mmm:</i>					
<i>Mmm-M</i> .....	.990	1.00	.96	.97	1.00
<i>Mmm-m</i> .....	.010	.00	.04	.03	.00
<i>Pgd1:</i>					
<i>Pgd1-2</i> .....	.303	.38	.33	.18	.05
<i>Pgd1-3.8</i> .....	.680	.59	.64	.82	.95
<i>Pgd1-n</i> .....	.017	.03	.02	.00	.00
<i>Pgd2:</i>					
<i>Pgd2-2.8</i> .....	.071	.21	.00	.00	.00
<i>Pgd2-5</i> .....	.929	.79	1.00	1.00	1.00
<i>Pgm1:</i>					
<i>Pgm1-9</i> .....	.978	1.00	.89	.97	1.00
<i>Pgm1-16</i> .....	.022	.00	.11	.03	.00
<i>Pgm2:</i>					
<i>Pgm2-1</i> .....	.002	.00	.00	.00	.00
<i>Pgm2-3</i> .....	.177	.05	.24	.23	.32
<i>Pgm2-4</i> .....	.754	.87	.73	.44	.68
<i>Pgm2-8</i> .....	.067	.08	.02	.33	.00
<i>Phil:</i>					
<i>Phil-2</i> .....	.012	.00	.07	.00	.00
<i>Phil-3</i> .....	.002	.00	.00	.00	.00
<i>Phil-4</i> .....	.837	.74	.78	1.00	1.00
<i>Phil-5</i> .....	.148	.26	.16	.00	.00

<sup>1</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the *Acp1* locus, *Acp1-2L* and *Acp1-2\** are variants of the *Acp1-2* allele. The *n* symbolizes a recessive null allele. The *R* at the *Me1* locus refers to the regularly found allele. At the *Mmm* locus, the *M* refers to the dominant and the *m* to the recessive forms of the two commonly found alleles.

<sup>2</sup>The publicly available lines most widely used as parents for hybrids planted in 1980 (Zuber and Darrah 1980). Each line was used as a parent for more than 1 million pounds of hybrid seed.



Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn

Allele <sup>1</sup> at locus--																						
LINE	Acpl	Adh1	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgm1	Pgm2	Phil
A	4	4	9	4	6	2	4	4	4	4	4	6	3.5	16	12	12	M	2	5	9	8	4
A1-6	2L	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
A3G-3-1-3	3#	n	7	4.5	6	6#	4	4	4	4	4.2	6	3	16	12	12	M	2#	5	9	4	2
A12	4	4	9	5	6	7	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	16	4	4
A90	4	4	9	4	6	2	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
A188	4	4	12	4.5	10	7	4	4	4	4	6	1	3.5	16	12	12	M	3.8	5	9	4	4
A239	3	4	9	5	6	2	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
A257	4	4	9	5	6	2	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
A295	2	4	9	4	6	6	4	4	4	6	6	6#	3	16	12	12	M	3.8	5	9	3	4
A297	4	4	9	4.5	6	7	4	4	4	4	4	6	3.5	16	12	12	M	2	5	9	4	4
A509	2	4	9	4	6	7	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
A554	2	4	9	5	6	7	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
A556	4	4	9	5	6	6	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
A619	4	4	9	4	6	6	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
A632	4	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
A634	4	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5#	9	4	5
A635	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
A639	4	4	9	4.5	6	2	4	2	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
A641	4	4	9	4	6	6	4	4	4	4	4	6	6	18	12	12	M	3.8	5	9	4	5
A654	4	4	9	5#	6	2	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
A656	4	4	9	4.5	6	2	4	2	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
A659	4	6	12	5	6	2	4	4	4	4	6	6	6	16	12	12	M	2	5	9	8	4
A661(A)	2&	4	9	4.5	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
A661(B)	4&	4	9	4.5	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
A665	4	4	9	5	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
A671	3	4	9	4.5	6	6	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
AA3	2	4	9	4.5#	6	7#	4	4	4	4	6	1	6	16	12	12	M	2	5	9	4	4
AA8	2	4	12	4	6	2	4	4	4	4	6#	6	6	16	12	12	M	2	5	9	4	4
AB408A	2	4	9	4	6	6	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	4
AY515-1-1	4	4	9	4	6	6	4	4	4	4	4	1	6	16	12	12	M	3.8	5	9	4	4
B4	4	4	9	4.5	6	6	4	4	4	4	4	6	6	18	12	12	M	2	5	9	4	4
B8	2	4	9	5	6	7	4	4	4	4	4	6	4.5	16	12	12	M	3.8	5	9	4	4
B9A(IA.)	4	4	9	4	6	7	4	4	4	4	6	6	3.5	18	12	12	M	2	5	9	3	4
B9A(MINN.)	4	4	9	5	6	7	4	4	4	4	6	6	6	18	12	12	M	2	5	9	3	4
B14A	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5

B37	2	4	9	5	6	7	4	4	4	4	4	6	6	6	6	16	12	12	M	2	5	9	4	4
B37R	2	4	9	5	6	7	4	4	4	4	4	6	6	6	6	16	12	12	M	2	5	9	4	4
B52	4	4	9	5	6	7	4	4	4	4	4	6	6	6	6	3.5	12	12	M	3.8	5	9	8	5
B57	2	4	9	5	6	7	4	4	4	4	4	6	6	6	6	3	12	12	M	3.8	5	9	4	4
B64	4	4	9	5	6	7	4	4	4	4	4	8	6	6	6	16	12	12	M	2	2.8	9	4	5
B68	3	4	9	5	6	7	4	4	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	5
B73	2	4	9	5	6	7	4	4	4	4	4	4	4	6	6	3.5	12	12	M	3.8	5	9	4	4
B75	3	4	9	5	6	2	4	4	4	4	4	4	4	6	6	3.5	12	12	M	2	5	9	3	4
B76	2	4	9	5	6	7	4	4	4	4	4	4	6	6	6	3.5	12	12	M	2	5	9	4	4
B77	4	4	9	4	6	2	4	4	4	4	4	4	6	1	6	16	12	12	M	3.8	2.8	9	4	5
B79	4	4	9	4.5	6	7	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
B84	4	4	9	5	6	7	4	4	4	4	4	4	4	6	6	3.5	12	12	M	2	5	9	3	4
C3	4	6	9	n	12	2	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
C11	6	4	9	4.5	6	2	4	4	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	4
C13	4	6	9	6	6	7	4	4	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4
C30	4	4	9	4	6	7	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
C103	3	4	9	4	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
C123	4	4	9	4.5	6	2	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
C1-29(A)	4	4	9	4	8	7	6	4	4	4	4	6#	6	6	3&	16	12	12	M	3.8	5	9	3	4
C1-29(B)	4	4	9	4	8	7	6	4	4	4	4	6#	6	6	6&	16	12	12	M	3.8	5	9	3	4
C6-29(A)	4	4	n	4	8	7#	6	4	4	4	4	4#	6	6	6&	16	12	12	M	3.8	5	9	3	4
C6-29(B)	4	4	n	4	8	7#	6	4	4	4	4	4#	6	6	3&	16	12	12	M	3.8	5	9	3	4
CG1	4	4	9	4	6	6	4	2	4	4	4	6	6	6	3.5	16	12	12	M	3.8	5	9	4	4
CG2	4	4	9	4	6	7	4	4	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
CG3	4	4	9	4	6	7	4	4	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
CG4	4	4	9	4.5	6	7	4	4	4	4	4	4	6	6	3	16	12	12	M	2	5	9	4	4
CG5	4	4	9	4	6	6	4	2	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
CG6	4	6	9	4	6	3	4	4	4	4	4	6	6	6	3.5	16	12	12	M	3.8	5	9	4	4
CG7	4	4	9	4.5	6	2	4	4	4	4	4	6	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CG8	4	4	9	4.5	6	7#	4	4	4	4	4	6	6	6	6	16	12	12	M	3.8	5	9	4	4
CG9	3	4	9	4	6	7	4	4	4	4	4	6	6	6	6	16	12	12	M	3.8	5	9	4	4
CG10	3	4	9	4	6	n#	4	4	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	5
CG11	4	4	9	5	6	7#	4	4	4	4	4	6	6	6	3	16	12	12	M	3.8	5	9	4	4
CG12	4	4	9	5	6	7	4	4	4	4	4	6	6	6	3	16	12	12	M	3.8	5	9	4	4
CG13	2	4	9	4.5	6	7	4	4	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	3	5

See footnote at end of table.

Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn—Continued

LINE	Allele <sup>1</sup> at locus—															
	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5
CG14	2	4	9	4.5	6	7	4	2	4	4	6	6	6	16	12	12
CG15	6	4	9	4	6	7	4	4	4	4	4	6	3.5	18	12	12
CH581-13	4	4	9	4.5	6	6	4	4	4	4	6	6	3.5	16	12	12
CH591-23	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
CH591-36	4	4	9	5	6	7	4	4	4	4	6	6	3.5	16	12	12
CH593-9	2	4	9	4.5	6	2	4	4	4	4	4	6	3.5	16	12	12
CH611-10	4	4	9	4.5	6	6#	4	4	4	4	6	6	3.5	16	12	12
CH665-1	4	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12
CH665-5	2#	4	9	4.5	6	6	6	4	4	4	6	6	6	16	12	12
CH671-28	4	4	9	4.5	6	6	4	4	4	4	6	6	3.5	16	12	12
CH701-30	4	4	12	4.5	6	n	4	4	4	4	6	6	3.5	16	12	12
CI.21E	4	4	9	4.5	6	1	4	4	4	4	4	6	3.5	16	12	12
CI.31	3	4	9	4.5	6	6#	4	4	4	4	6	6	3.5	18	12	12
CI.38B	2	4	9	4.5	6	7	4	4	4	4	4	6	3	16	12	12
CI.44	4	4	9	4	6	9	4	4	4	4	4	6	3	16	12	12
CI.45	2	4	9	4.5	6	2	4	4	4	4	6	6	3	16	12	12
CI.64	3	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12
CI.66	4	4	9	4	4	7	4	4	4	4	6	6	6	16	12	12
CI.90A	4	4	9	4.5	6	n	4	4	4	4	4	6	3.5	16	12	12
CI.127	4	4	9	5	6	2	4	4	4	4	4	6	3	16	12	12
CI.187-2	2	6	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12
CI.540	4	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
CK22	4	6	9	4.5	6	6	4	4	4	4	6	6	3	16	12	12
CK25	4	4	9	5	6	2	4	4	4	4	4	6	3.5	16	12	12
CK26	2	4	9	5	6	2	4	4	4	4	4	6	3	16	12	12
CK27	2	6	9	4#	6	7#	4	4	4	4	6	6	3	16	12	12
CK29	6	4	9	4	6	2	4	4	4	4	4	6	3.5	18	12	12
CK36	2#	4	9	5	6	2#	4	4#	4	4	6#	6	3	16	12	12
CK43	2	4	9	5	6	7	4	4	4	4	6	6	3	16	12	12
CK48	2	4	9	4.5	6	7	4	2	4	4	6	6	6	16	12	12
CK52	4	4	7	5	6	7	4	4	4	4	6	6	3	16	12	12
CK54	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12
CK55	2	4	9	5	6	7	4	4	4	4	6	6	3	16	12	12
CK63	4	6	9	4.5	6	7#	4	4	4	4	4	6	6	18	12	12
CK64	2	4	9	5	6	2	4	4	4	4	6	6	3	18	12	12

CK71	2	6	9	4	6	2	4	4	2	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
CM7	4	4	12#	4	6	7	4	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	3	4
CM37	2	6	9	4.5	6	7	4	4	2	6	6	6	6	3.5	16	12	12	M	3.8	5	9	3	5
CM105	4	4	9	5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CM109	4	4	9	5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CM113	4	4	9	5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CM139	2	4	9	5	6	2	6	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	5
CM151	4	4	9	5	6	7	6	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	5
CM169	4	4	9	5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CM174	4	4	9	4.5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	4
CMD5	4	4	9	4.5	6	6	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
CMV3	2	4	9	5	6	7	4	4	4	4	4	6	6#	3	16	12	12	M	3.8	5	9	3	4
CO106	4	4	9	4.5	6	6	4	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
CO109	4	4	9	4	6	3	4	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
CO113	4	4	9	4.5	6	6	4	4	2	4	4	4	6	6	18	12	12	M	2	5	9	4	4
CO125(A)	4	4&	9#	4	6	n#	4	4	4#	4	4	4#	6	3.5#	18#	12	12	M	3.8	5	9	3#	4
CO125(B)	4	6&	9#	4	6	n#	4	4	4#	4	4	4#	6	3.5#	18#	12	12	M	3.8	5	9	3#	4
CO150	2	6	9	4.5	6	7	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
CO158	4	4	9	4.5	6	1	4	4	4	4	6	6	6	3	18	12	12	M	3.8	5	9	4	4
CO159	3	6	9	5	10	6	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
CO220	4	4	9	4	6	3	4	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
CQ160	4	6	9	4	6	6	4	4	4	4	4	6	1	6	16	12	12	M	3.8	5	9	4	4
CQ165	4	4	9	5	10	6	6	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	5
CQ177	4	4	9	4.5	6	1	4	4	4	4	4	6	6	6	18	12	12	M	3.8	5	9	4	4
CQ178	4	4	9	4.5	6	1	4	4	4	4	4	6	6	3	18	12	12	M	3.8	5	9	4	4
CQ179	4	4	9	4.5	6	1	4	4	4	4	4	6	6	3	18	12	12	M	3.8	5	9	4	4
CQ180	4	4	9	4	6	2	4	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
CQ181	2	4	9	5	6	6	6	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	5
CQ182	2	4	9	4	6	6	4	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	5
CQ184	4	4	9	4	6	3#	4	4	2#	4	4	6#	6	6	16	12	12	M	3.8	5	9	4	4
CQ184A	4	4	9	4.5	6	3	4	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
CQ187	2	4	9	5	6	7	4	4	4	4	4	4	6	6	16	12	12	M	3.8	2.8	9	3	5
CQ188	2	4	9	5	6	7	4	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	3	5
CQ193	4	4	9	4.5	6	1	4	4	2	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
CQ197	4	4	9	4.5	6	6	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4

See footnote at end of table.

Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn—Continued

Allele <sup>1</sup> at locus--																						
LINE	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgm1	Pgm2	Phil
CQ198A	4#	6#	9	5	6	6#	4#	4	4	4	4#	1	3.5#	16	12	12	M	3.8	5	9	4	4
CQ200	3	4	9	5	6	6	6	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
CQ201	3	4	9	5	6	7	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
CQ205	2	4	9	4	6	2	6	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
CQ207	2	4	9	4	6	6	6	4	4	4	6	6	3.5	16	n	12	M	2	5	9	4	5
CQ209	2	4	12	5	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
CQ214	4	4	9	4	6	3	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	5
CQ707	2	4	9	5	6	7	6	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
EP1	4	4	9	4.5	6	2#	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
FF2	2	6	9	4.5	6	7	4	4	4	4	4	6	6	16	12	15	M	3.8	5	9	1	4
FF6	4	4	9	4.5	6	n#	4#	4	4	6#	4	6	6	16	12	12	M	3.8	5	9	4	5
FF7	3	4	9	4	6	7	4	4	4	6	4	6	3	16	12	12	M	2	5	9	4	4
FF44	2*#	4	9	4.5	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
FE-2	2	4	9	4.5	6	2	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4
FL32	4	4	12	4	6	7	4	4	4	4	6	6	6	16	12	12	M	2	5	9	8	4
FL56	4	4	9	4	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
GA209	2#	4	9	5	6	2	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	3	5
GT112	3	6	9	4.5	6	7	4	4	4	4	4	1	3	16	12	12	M	2	5	9	4	5
H21	4	4	12	4.5	4	2	4	4	4	4	6	6	3.5	16	12	12	M	n	5	9	4	4
H25	3	6	9	4.5	6	2	4	4	4	4	6	n	3	18	12	12	M	3.8	5	9	4	4
H30	2	4	9	4.5	6	7	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
H49	3	4	9	5	6	6	6	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
H60	3	4	9	4.5	6	7	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
H84	2	4	9	5	6	6	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
H91	4	4	9	5	6	7#	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
H93	2	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	4
H95	4	4	9	4	6	n	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
H96	2	6#	9#	4	6	6#	4	4	4	6	4	6	3#	16	12	12	M	3.8	5	9	3#	4
H98	2	4	9	5	6	6	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
H99	2	4	9	4.5	6	6	4	4	4	4	6	6	3	16	12	12	M	n	5	9	4	4
H100	2	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
H5505	3	6	n	4.5	8	7	6	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
HI25	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	2.8	9	4	5
HI30	2	4	12#	5	6	2#	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
PP62-49	2	4	n	4	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4



HP301	2	4	9	4	9	4	6	7	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
HP302	2	4	9	4	9	4	6	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
HP304W	2	4	9	4	9	4	6	6	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
HY	2	6	9	5	6	4	6	6	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
I29	2	4	n	4.5	8	7	4	7	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
I159	4	6	9	5	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	16	3	4
I205	4	6	9	5	6	6	4	6	4	4	4	4	4	4	4	6	1	3.5	16	12	M	2	5	9	4	4
I224A2	4	4	9	5	6	6	4	6	4	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
IA453	4	4	9	4	6	7	4	7	4	4	4	4	4	4	4	6	10.5	6	16	12	M	3.8	5	9	8	4
IA2132	4	4	12	4	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	8	4
IA2256	4	4	9	4	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
IA5125B	4	6	n	4.5	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
IDS28	2	4	n	4.5	6	n#	4	n#	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
IDS69	2	4	9	4	6	7	4	7	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
IDS91	2	4	9	4	6	7	4	7	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
IL11A	4	6	9	4	6	2.5	4	2.5	4	4	4	4	4	4	4	4	10.5	3	16	12	M	3.8	5	9	3#	4
IL13B	4	4	9	4	6	7	4	7	4	4	4	4	4	4	4	4	10.5	6	16	12	M	3.8	5	9	3	4
IL14H	4	n#	n	4	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
IL18B	4	6	9	4	10	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
IL27A	3	6	9	4	10	7	4	7	4	4	4	4	4	4	4	4	10.5	6	16	12	M	3.8	5	9	8	4
IL101T	4	6	n	4	6	6	4	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
IL110G	4	6	9	4	6	7	4	7	4	4	4	4	4	4	4	6	6	6#	16	12	M	3.8	5	9	4	4
IL442A	4	4	12	4	6	1	4	1	4	4	4	4	4	4	4	6	10.5	6	16	12	M	2	5	9	4	4
IL451B	4	4	9	4	6	6	4	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
IL671A	4	4	9	4	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
IL677A	4	4	12	4.5	n	1	4	1	4	4	4	4	4	4	4	6	10.5	6	16	12	M	3.8	5	9	3	4
IL685D	2	4	9	4.5	6	2	4	2	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
IL731A	4	4	9	4.5	n	1	4	1	4	4	4	4	4	4	4	6	10.5	6	16	12	M	3.8	5	9	3	4
ILL-12E	4	4	9	4.5	6	2#	4	2#	4	4	4	4	4	4	4	6	6	16	12	15	M	2	5	9	4	4
ILL-HY	3	6	9	5	6	6	4	6	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
IND461-3	4	4	9	4.5	6	6	4	6	4	4	4	4	4	4	4	4	6	6	18	12	M	2	5	9	4	4
IND-A.H83	2	4	9	4.5	6	7	4	7	4	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
IND-B2	2	4	9	4.5	6	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
IND-TR9-1	4	4	9	5	6	7	4	7	4	4	4	4	4	4	4	6	6	3.5	16	12	M	2	5	9	4	4
K6	2	4	9	5	8	7	4	7	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4

See footnote at end of table.

Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn—Continued

LINE	Allele <sup>1</sup> at locus--																					
	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgml	Pgm2	Phl1
K41	2	4	12	5	n	7	4	4	4	4	6	6	3.5#	16	12	12	M	3.8	5	9	4	4
K55	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	n	M	3.8	5	9	4	4
K64	3	4	12	4.5	6	7	4	4	4	4	6	6	n	16	12	12	M	3.8	5	9	4	4
K148	2	4	9	4.5	6	7	4	4	4	4	6	6	3	16	12	12	M	n	5	9	4	5
KP39	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	3	4
KP58K	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	3	4
KY21	3	4	9	5	6	7	4	4	4	4	6	1	n	16	12	12	M	3.8	5	9	3	4
KY201	3	4	n	4	4	7	4	4	4	4	6	1	3	16	12	12	M	3.8	5	9	4	5#
KY216	4	4	9	5	8	7	6	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
KY225	2*	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	5
KY226	3	4	9	5	6	6	6	4	4	6	4	6	3.5	16	12	12	M	3.8	5	16	4	4
KY228	2#	4	9	4.5	6	2	4	4	4	4	6	6	6	16	12	12	m	2	5	9	4	4
L289	4	4	9	5	6	7	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
L317	4	4	9	4	6	7	4	4	4	4	4	1	6	16	12	12	M	3.8	5	9	4	4
LE23	2	6	9	4	6	7	4	2	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
M14	4	4	9	4.5	6	7#	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4
M49	4#	4	12	4	6	7	4	4	4	4	6	6	4.5	16	12	12	M	3.8	5	9	4	4
MA20	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
MAC5NT	4	6	9	4	6	7	4	2	4	4	6	6	6	16	12	12	m	3.8	5	16	3	4
ME2RT	4	6	9	4	6	7	4	4	4	4	4	10.5	6	16	12	12	M	3.8	5	9	4	4
MEF156-55	4	6	9	4	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	3	4
MICH6	4	4	9	4.5	6	n	4	4	4	4	4	1	3	16	12	12	M	2	5	9	4	4
MICH37W	4	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	5
MICH37Y	4	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	5
MICH59	4	4	9	4.5	6	n	4	4	4	4	4	10.5	3.5	16	12	12	M	2	5	9	4	5
MICH77	4	6	9	5	6	7	4	4	4	4	6	6	3	16	12	12	M	2#	5	9#	4#	4
MICH77-5	4	4	9	4.5	6	6	4	4	4	4	4#	6	3.5#	16	12	12	M	2	5	9	4	4
MICH77-6	2	4	9	4.5	6	n	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
MICH77-7	4	4	9	4.5	6	6	4	4	4	4	4#	6	3#	16	12	16.4#	M	3.8	5	9	4	4
MICH77-8	4	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	4
MICH77-9	4	4	9	4	6	6	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	4
MICH77-10	4	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
MICH81	4	4	9	4.5	6	2	4	4	4	4	6	1	3	16	12	12	M	3.8	5	9	4	4
MO1W	2	6	9	5	6	6	6	4	4	4	4	6	3	16	12	12	M	2	5	16	4	4
MO5	4	4	9	4	6	7	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4

M06	3	4	4	9	4.5	6	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
M07A	2	4	4	9	4	6	7	4	4	4	4	4	4	4	4	6	6	16	12	12	M	n	5	9	4	4
M012	2	4	4	9	4.5	6	6	6	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
M013	4	4	4	9	4	6	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
M014W	2	4	4	9	4.5	6	2	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
M017	2	4	4	9	4	6	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
M018W	2	6	9	9	4.5	6	6	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	16	4	4
M020W	2	6	9	9	4.5	6	1	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	16	4	4
M023W	4	4	4	9	4	10	2	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
M024W	4	4	4	9	4	6	7#	4#	4	4	4	4	4	4	4	6	1	16	12	12	m	2	5	16	3	4
M025W	4#	4	4	9	4.5	4	7#	4	2	4	4	4	4	4	4	4	1	3	16	12	M	3.8	5	9	3#	4
M040	2	4	4	9	4	6	6	4	4	4	4	4	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
M041	3	4	4	9	4	6	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	5
M042	2	4	4	9	4	6#	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
M043	2	4	4	9	4	6	6	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
M0505W	3	6	9	9	4	6	2	4	4	4	4	4	4	4	4	6	n	18	12	12	M	3.8	5	9	4	4
M0510W	3	4	4	9	4	6	7	6	4	4	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	3	4
MP305	4	4	4	9	4.5	n	6	4	4	4	4	4	4	4	4	1	6#	16	12	12	M	2	5	9	3	4
MP307	2	4	4	12	4	6	7	4	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
MP311	3	6	9	9	4.5	6	7	4	4	4	4	4	4	4	4	1	3	16	12	12	M	2	5	9	4	4
MP339	2	4	4	9	5	6	7	4	4	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
MP444	3	4	4	9	4.5	6	1	4	4	4	4	4	4	4	4	6	3	18	12	12	M	2	5	9	4	4
MP462	4	4	4	9	4.5	6	7	4	4	4	4	4	4	4	4	6	6	18	12	12	M	2	5	9	4	4
MS80	4	4	4	9	4	6	2#	4	4	4	4	4	4	4	4	6	3.5#	16	12	12	M	3.8	5	9	8	4
MS92	4	4	4	9	4	6	7#	4	4	4	4	4	4	4	4	6	1	16	12	12	M	3.8	5	9	4	5
MS153	4	4	4	9	5#	6	7	4	4	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4#	4
MS1334	4	4	4	9	4	6	n#	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
MT42	6	4	4	12	4.5	6	2	6	4	4	4	4	4	4	4	6#	3.5	18	12	12	M	2	5	9	4	5
N6	2	6	9	9	5	6	1	4	4	4	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
N7A	4	4	4	9	4.5	6	1	4	4	4	4	4	4	4	4	6	6	16	12	12	M	2	2.8	9	4	4
N15	4	4	4	9	5	6	6	4	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
N28	2	4	4	9	4.5	6	7	4	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4#
N132	2	6#	9	9	4.5	6	1	4	4	4	4	4	4	4	4	6	3#	16	12	12	M	2#	5	9	4	4
N152	2	4	4	9	4.5	6	1	4	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8#	5#	9	4	4
N159	2#	4	4	9	5	6	6	6	4	4	4	4	4	4	4	6	3.5#	16	12	12	M	2	5	9	4	4

See footnote at end of table.

Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn—Continued

LINE	Allele <sup>1</sup> at locus--																					
	Acpl	Adh1	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgm1	Pgm2	Phil
N160	4	4	9	4.5	6	7#	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
NC7	4	4	9	4	6	1	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	5
NC234	4	4	9	4	6	6	4	2	4	4	4	6	6	16	12	12	M	2	5	9	4	4
ND203	2	4	9	4	6	6	4	4	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
ND240	4	4	9	4.5	6	2	4	2	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
ND408	4	4	9	4.5	6	7	4	2	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
ND474	2	4	9	5	6	10	6	4	4	4	6	6	3	16	12	12	M	2	5	9	4	4
NY303	4	4	n	4	6	3#	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	3	4
NY821	4	4	9	4.5	6	6	4	2	4	4	4	6	3.5	16	12	12	M	n	5	9	4	4
NYP501	3	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
OH07	4	4	9	4.5	6	1	4	4	4	4	4	6	6	16	12	12	M	3.8	2.8	9	4	4
OH7B	4	4	9	4.5#	6	1	4	4	4	4	4	6	6	16	12	12	M	3.8	2.8	9	4	4
OH40B	4	4	9	4.5	6	7	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	4	4
OH43	4	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
OH51A	4	4	9	4.5	6	n#	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
OH514	4	4	9	4.5	6	10	4	4	4	4	6	6	3	16	12	12	M	3.8	2.8	9	4	5
OH545	4	4	9	4.5	6	6	4	2	4	4	4	6	6	18	12	12	M	3.8	5	9	4	4
OH551	4	4	9	4.5	6	7#	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
OH3167B	3	6	9	5	6	7	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4
OS420	4	4	9	5	6	7	4	4	4	4	4	6	3	16	12	12	M	3.8	5	9	4	4
P39(ROBSN)	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4
P39(CROOK)	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
P51T	4	6	n	n	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	4	4
PA71-U6	3	6	12	4#	10	7#	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	3	4
PA32	2#	4	12#	4#	6	2#	6#	4#	4	4	4	1#	3#	16	12	12	M	2#	5	9	3#	5#
PA33	2	4	9	4	6	2	4	4	4	6	6	6	6	16	12	12	M	2	5	9	4	4
PA91	4	4	9	4.5	6	7	4	4	4	4	4	6	3.5	16	12	12	M	2	5	9	4	4
PA762	4	4	9	4.5	6	6	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	4	4
PA884P	3	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	4
R4	2	4	9	4.5#	6	7	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	3#	4
R95	4	4	9	4.5	6	7	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	4	2
R168	4	4	12	4.5	6	7	4	4	4	4	6	1	3.5	16	12	12	M	3.8	2.8	9	4	4
R177	4	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
R181B	2	4	9	5	6	7	4	4	4	4	6	1	6	16	12	12	M	3.8	5	9	4	4
R806(A)	4#	4	12	4	6	7	4	4	4	4	6	6#	3	16	12	15&	M	3.8	5	9	4	4

R806(B)	4#	4	12	4	6	7	4	4	4	4	4	4	6	6#	3	16	12	12&	M	3.8	5	9	4	4
R825	4	6	n	4.5	6	7	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4
R839	4	4	9	6	6	7	4	4	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4
R853	4	4	9	4	6	7	4	4	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4
S4	4	6	9	4	6	7	4	4	2	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
S8	4	6	9	4	6	7	4	4	2	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4
SA24	2	4	9	4	6#	7	4	4	4	4	4	4	4	6#	3.5	16	12	12	M	3.8	5	9	4	4
SC55	2	4	9	4.5#	6	2	4	4	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	8	5
SC213R	2#	4	12#	4.5	6	7	4	4	4	4	4	4	4	1	3	16#	12	12	M	2	5	9	4	5
SC246C	2*	4	9	5	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
SC344	4	4	12	4#	10	6	4	4	4	4	4	4	4	6	3	18	12	12	M	3.8	5	9	3	5
SC359	3	4	9	4.5	6	1	4	4	4	4	4	4	4	1	3.5	16	12	12	M	3.8	5	9	4	4
SD5	4	4	9	4	6	7	4	4	4	4	4	4	4	6	3.5	16	12	12	M	2	5	9	4	4
SD10	2	4	9	5	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
SD15	2	4	9	4	6	6	4	4	4	4	4	4	6	6	3.5#	16	12	12	M	2	5#	9	4#	4
SG16	2	4	9	4.5	6	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
SG18	2	4	9	4	6	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4#	4
SG1533	2	4	9	4.5	6	7	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
T8	4	4	9	4	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	5
T13	4	4	9	4.5	8	7	4	4	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	3	4
T61	2	4	9	5	6	7	4	4	4	4	4	4	4	6#	3	16	12	12	M	3.8	5	9	3	5
T101	4	4	9	4	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
T111	2	4	9	4.5	6	6	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
T115	2	4	9	6	6	7	4	4	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	3	4
T139	2	4	9	6	6	7	4	4	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	3	4
T204(A)	4	4	9	4	6	6&	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
T204(B)	4	4	9	4	6	n&	4	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
T220	2	4	12	5	6	7	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	5
T220A	2	4	12	5	6	7	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	5
T224	4	4	9	6	6	6#	4	4	4	4	4	4	4	1	3.5	16	12	12	M	2	5	9	3	4
T226	2	4	12	4.5	6	6	6	4	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
T232	4	4	9	4	6	2	4	4	4	4	6	4	4	1	6	18	12	15	M	3.8	2.8	9	4	4
TX61M(A)	4	4	9	4.5	6	7	4	4	4	4	4	4	4	1&	3	16	12	12	M	3.8	5	9	4	2
TX61M(B)	4	4	9	4.5	6	7	4	4	4	4	4	4	4	6&	3	16	12	12	M	3.8	5	9	4	2
TX203-2	3	4	9	5	6	7	4	4	4	4	4	4	4	6	3	16	12	12	M	2	5	9	4	4

See footnote at end of table.



Table 5.—Allozyme genotypes of 406 U.S., Canadian, and European inbred lines of corn—Continued

LINE	Allele <sup>1</sup> at locus--																					
	Acpl	Adh1	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgml	Pgm2	Phil
TX303	4	4	9	4#	6	7	4	4	4	6	6	6	3	18	14.5	n	M	2	5	9	3	2
TX325	4	6#	9	5#	6	6#	4	4	4	4	6	6	3	16	14.5#	n	M	2#	5	9#	3	4#
TX585	3	4	9	5	6	2	4	4	4	6	6	6	6	16	12	12	M	2	5	9	4	4
TX601(A)	3	4	9	4.5	6	2&	6#	4	4	4	6	6	6#	16	12	12	M	n	5	9	4	4
TX601(B)	3	4	9	4.5	6	n&	6#	4	4	4	6	6	6#	16	12	12	M	n	5	9	4	4
TX6252	4	4	9	4	6	6	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	3
VA17	4	4	9	4	6	6	4	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
VA26	4	4	9	4.5	6	6	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
VA32	2	4	9	5	6	6	6	4	4	4	6	6	3.5	16	12	12	M	2	5	9	4	4
VA35	4	4	9	4	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	5
VA36	3	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
VA50	4	6	9	5	6	6	4	4	4	4	4	1	3.5	18	12	12	M	3.8	5	9	4	4
VA58	4	4	9	4	6	7	4	4	4	4	4	1	6	16	12	12	M	3.8	5	9	4	4
VA59	4	4	9	5	6	6	4	4	4	4	4	1	6	16	12	12	M	3.8	5	9	4	4
VA60	4	4	9	4.5	6	6	4	2	4#	4	4	6	6	16	12	12	M	3.8	5	9	4	4
VA61	3	4	9	4	6	6	4	4	4	4	4	1	6	16	12	12	M	3.8	5	9	4	4
VA85	3	4	12	4	6	6	4	4	4	4	4	1	5.6	18	12	12	M	3.8	5	9	4	4
VA94	4	4	9	5	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4
VA-79:419	2	4	9	4.5	6	1	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	4
W22	3	4	9	5	6	7	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	5
W59E	2	4	9#	5	6	7	4	4	4	4	6	6	6	16	12	12	M	2#	5	9	3	4
W59MHT(A)	2	4	12	5	6	7#	4	4	4	4	6	6	6	16&	12	12	M	3.8#	5	9	3	4
W59MHT(B)	2	4	12	5	6	7#	4	4	4	4	6	6	6	18&	12	12	M	3.8#	5	9	3	4
W64AHT	2	4	9	4.5	6	6	6	4	4	4	6	6	6	16	12	12#	M	2	5	9	8	4
W83	4	4	9	5	6	2	4#	4	4	4	4	6	3.5	16	12	12	M	2	5	9	4	4
W117HT	2	4	9	4.5	6	7#	4	4	4	4	6	1	3	16	12	12	M	2	5	9	4	4
W153RHT	6	4	9	4.5	6	6	4	4	4	4	6	6	6	18	12	12	M	3.8	5	9	3	4
W182B	2	4	9	5	6	10	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	5#
W182BHT(A)	2	4	9	5	6	10#	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	4&
W182BHT(B)	2	4	9	5	6	10#	4	4	4	4	6	6	3	16	12	12	M	3.8	5	9	4	5&
W375B	2	4	9	5	6	2	4	4	4	4	4	6	3#	16	12	12	M	3.8	5	9	3#	4
W401	2	4	9	5	6	7	4	4	4	4	6	6	4.5	16	12	12	M	2	5	9	3	4
W438	2#	4	9#	4.5#	6	7	4	4	4	4	6	6	3	16	12	12	M	2	5	9	3#	4
W462	3	4	9	5	6	7	4	4	4	4	6	6	3.5	16	12	12	M	3.8	5	9	4	5
W538	3	4	12	4	6	7	4	4	4	4	4	6	3.5	16	12	12	M	3.8	5	9	4	4

W540	4	4	9	5	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	5
W544	2	4#	9	5	6	7#	4	4	4	4	4	6	6	16	12	12	M	3.8	2.8	9	4	4#
W546(A)	4	4	9	5	6	6&	4	4	4	4	4	6	3.5	16	12	12	M	2	2.8	9	4	4
W546(B)	4	4	9	5	6	7&	4	4	4	4	4	6	3.5	16	12	12	M	2	2.8	9	4	4
W629A	2	4	9	5	6	2	4	4	4	4	4	6	6	16	12	12	m	3.8	5	9	4	4
W703	2	4	9	5	6	6	4	4	4	4	4	6	10.5	6	16	12	M	2	5	9	4	5
W705A	4	4	9	4.5	6	7	4	4	4	4	4	4	6	3.5	16	12	M	3.8	5	9	4	4
W729C	3	6	9	5	6	1	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	5
W729D(A)	3&	6#	9	5	6	1	4	4	4	4	4	4	6	3.5	16	12	M	3.8	5	9	4	5
W729D(B)	6&	6#	9	5	6	1	4	4	4	4	4	4	6	3.5	16	12	M	3.8	5	9	4	5
W845	2	4	12	5	6	7	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	4
WD	2	4	9	5	6	10	4	4	4	4	4	6	6	3	16	12	M	3.8	5	9	4	4
WD456	4	4	9	4.5#	6	6	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	4
WF9	2	4	9	5	6	6	4	4	4	4	4	6	3.5	16	12	12	M	2	5	9	4	4
WJ	3	4	9	4.5	6	1	4	4	4	4	4	4	6	16	12	12	M	2	5	9	4	4
33-16	2	4	9	5	4	7	4	4	4	4	4	6	6	3	16	12	M	2	5	9	4	5
38-11	2	4	9	4.5	6	7	4	4	4	4	4	4	6	3	16	12	M	3.8	5	9	4	4
81-1	2*	6	9	4	6	2	4	4	4	4	4	4	6	6	16	12	M	3.8	5	9	4	4
442	2	4	12	4#	6	7	4	2	4	4	4	6	6	16	12	12	M	2	5	9	4	4
4722	4	4	12	4	6	6	4	4	4	4	4	4	6	3.5	16	12	M	2	5	9	4	4
4C082	3	4	9	4	6	7	4	4	4	4	4	6	10.5	n	16	12	M	3.8	5	9	3	5

<sup>1</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

Table 6.—Allozyme genotypes of 15 Latin American and Indian inbred lines of corn

LINE	Allele <sup>1</sup> at locus--																					
	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idhl	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mmm	Pgd1	Pgd2	Pgml	Pgm2	Phil
CM103(A)	2#	4	9	4.5	6#	2#	4	4	4	4	4#	1#	6	16	12	12	M	2#	5	9	3&	4
CM103(B)	2#	4	9	4.5	6#	2#	4	4	4	4	4#	1#	6	16	12	12	M	2#	5	9	4&	4
CM104(A)	3	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	2#	5	9	3&	5
CM104(B)	3	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12	M	2#	5	9	4&	5
CM105(A)	2#	4	9#	4#	6	7	4	4	4	4	4#	6	3&	16	12	12	M	3.8#	5	9	4	4
CM105(B)	2#	4	9#	4#	6	7	4	4	4	4	4#	6	6&	16	12	12	M	3.8#	5	9	4	4
ETOB2053	4	4	9	4.5	6	2	4	4	4	4	4	1	6	16	12	16.4#	M	3.8	5	9	3	4
L.25	3	4	9	4.5	6	2	4	4	4	4	4	6	6	16	12	12	M	2	5	9	3	4
L.26	3	4	9	4.5	6	2	4	4	4	4	4	1	6	16	12	12	M	2	5	9	8	4
L.27(A)	4#	4	9	4.5	6	2#	4	4	4	4	4	1#	3&	16	12	12#	M	3.8	5	9	3	4
L.27(B)	4#	4	9	4.5	6	2#	4	4	4	4	4	1#	6&	16	12	12#	M	3.8	5	9	3	4
L.28	4	4	9	4.5	6	2	4	4	4	4#	4	6	6	16	12	12	M	3.8	5	9	3	4
L.29	4	4	9	4.5	4#	2#	4	4	4	4	4	6	3#	16	12	12	M	2	5	9	4	4
L.36	2	4	9	4.5	6	2#	4#	4	4	4	4	6	3#	16	12	12	M	3.8#	5	9	3	4
L.210	2#	4	9	4.5	6	2#	4	4	4	4	4#	6	3	16	12	15#	M	2#	5	9	4	4

<sup>1</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

studied additional collections from Latin America. Of the 245 alleles that we have identified, we found 80 in the 406 popular and historically important U.S., Canadian, and European inbred lines surveyed for this study (tables 3 and 4).

## ALLOZYME GENOTYPES OF THE ENTIRE SET

Allozyme genotypes (fingerprints) for the entire set of publicly available inbred lines studied are presented in tables 5 and 6. (The 15 Latin American and Indian lines shown in table 6 are not considered further in this paper because most are not well adapted to U.S. corn-growing areas.) Because most lines are homozygous, only a single number is listed for each locus in these tables and in tables 8-11.

Fifteen of the 391 differently named lines in table 5 are listed twice for the total of 406. Twelve of these double listings (for A661, C1-29, C6-29, CO125, R806, T204, Tx61M, Tx601, W59MHt, W182BHt, W546, and W729D) occur because these lines showed two equally frequent alleles at one locus and were treated as two lines each, designated by the letters A and B. So, for example, A661 is listed as A661(A) and A661(B). The

other 3 double listings came about because, of the 10 lines obtained from 2 different sources, 3 had 2 distinct genotypes for each line. These, then, are listed as B9A(Ia.) and B9A(Minn.), Hy and Ill.Hy, and P39(Robsn) and P39(Crook). The other seven lines obtained from two different sources (B37, C13, CI.187-2, F44, Ga209, P471-U6, and 33-16) had identical genotypes.

For the 23 loci evaluated, we detected 80 alleles (table 3). Only two loci, *Got3* and *Me1*, were monomorphic, and the *Glu1* locus had nine different alleles. For the entire set of 406 lines, we found 342 (84%) different genotypes; 295 (73%) of the lines were unique within the set (table 7). A line is defined as being unique if its genotype is different from that of any other line in the set. Groups of lines that had identical electrophoretic patterns are listed on p. 23. In only about 25% of these groupings are more than two lines alike. In many instances, published pedigrees (Henderson 1976, 1980) show that the members of these sets are very closely related. For example, Va35, which shares an identical genotype with T8, was derived from the cross C103  $\times$  T8 backcrossed to T8. Also, Ind-B2, one of the original components of Stiff Stalk Synthetic, has a genotype that is identical with that of N28, a line derived from that synthetic.

Table 7.—Relative uniqueness in the entire set and 4 subsets of 406 U.S., Canadian, and European inbred lines of corn

Set of lines	Number of lines in set <sup>1</sup>	Distinct genotypes within set		Lines unique within set		Lines unique to entire set	
		Number	Percent	Number	Percent	Number	Percent
Entire . . . . .	406 (391)	342	84	295	73	295	73
Widely used <sup>2</sup> . . . .	39 (39)	36	92	33	85	26	67
White corn . . . . .	45 (44)	43	96	41	91	37	82
Sweet corn . . . . .	39 (38)	32	82	26	67	25	64
Popcorn . . . . .	22 (20)	16	73	13	59	13	59

<sup>1</sup>The number in parentheses is the number of differently named lines in each set.

<sup>2</sup>The publicly available lines most widely used as parents for hybrids planted in 1980 (Zuber and Darrah 1980). Each line was used as a parent for more than 1 million pounds of hybrid seed.



Table 8.—Allozyme genotypes of the 39 most widely used<sup>1</sup> of 406 U.S., Canadian, and European inbred lines of corn

LINE	Allele <sup>2</sup> at locus--															
	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5
A554	2	4	9	5	6	7	6	4	4	4	6	6	3	16	12	12
A619	4	4	9	4	6	6	4	4	4	4	6	6	3	16	12	12
A632	4	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12
A634	4	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12
A635	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
A654	4	4	9	5 <sup>#</sup>	6	2	4	4	4	4	6	6	3.5	16	12	12
A656	4	4	9	4.5	6	2	4	4	4	4	6	6	3	16	12	12
A659	4	6	12	5	6	2	4	4	4	4	6	6	6	16	12	12
A665	4	4	9	5	6	6	4	4	4	4	6	6	6	16	12	12
B14A	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
B37	2	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
B64	4	4	9	5	6	7	4	4	4	8	6	6	6	16	12	12
B68	3	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
B73	2	4	9	5	6	7	4	4	4	4	4	6	3.5	16	12	12
B84	4	4	9	5	6	7	4	4	4	4	4	6	3.5	16	12	12
CI.64	3	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12
CI.66	4	4	9	4	4	7	4	4	4	4	6	6	6	16	12	12
CM105	4	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
CO109	4	4	9	4	6	3	4	2	4	4	6	6	6	16	12	12
CO220	4	4	9	4	6	3	4	2	4	4	6	6	6	16	12	12
H49	3	4	9	5	6	6	6	4	4	4	4	6	3	16	12	12
H84	2	4	9	5	6	6	4	4	4	4	4	6	6	16	12	12
H93	2	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
H95	4	4	9	4	6	n	4	4	4	4	6	6	6	16	12	12
H99	2	4	9	4.5	6	6	4	4	4	4	6	6	3	16	12	12
H100	2	4	9	5	6	7	4	4	4	4	6	6	6	16	12	12
K55	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	n
MO17	2	4	9	4	6	6	4	4	4	4	4	6	6	16	12	12
N7A	4	4	9	4.5	6	1	4	4	4	4	6	6	6	16	12	12
N28	2	4	9	4.5	6	7	4	4	4	4	6	6	6	16	12	12
OH43	4	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	12
PA91	4	4	9	4.5	6	7	4	4	4	4	4	6	3.5	16	12	12
PA762	4	4	9	4.5	6	6	4	4	4	4	4	1	3	16	12	12
SC213R	2 <sup>#</sup>	4	12 <sup>#</sup>	4.5	6	7	4	4	4	4	4	1	3	16 <sup>#</sup>	12	12
T220	2	4	12	5	6	7	4	4	4	4	4	6	3	16	12	12



VA26	4	4	9	4.5	6	6	6	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4
W64AHT	2	4	9	4.5	6	6	6	4	4	6	6	6	16	12	12#	M	2	5	9	8	4
W117HT	2	4	9	4.5	6	7#	4	4	4	6	1	3	16	12	12	M	2	5	9	4	4
W153RHT	6	4	9	4.5	6	6	6	4	4	6	6	6	18	12	12	M	3.8	5	9	3	4

<sup>1</sup>The publicly available lines most widely used as parents for hybrids planted in 1980 (Zuber and Darrah 1980). Each line was used as a parent for more than 1 million pounds of hybrid seed.

<sup>2</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

#### Groups of lines with identical electrophoretic patterns

A257	CG11	FL56	Mich37W
CI.127	CG12	IA2256	Mich37Y
A297	CG14	HP301	Mo17
Pa91	CK48	IDS69	Mo42
A635	CH665-1	IDS91	
B14A	Mich77-8	SA24	Mo40
H91		HP302	ND203
Hi25	CI.38B	SG16	N159
	H30	SG1533	Va32
A639	Ind-A.H83		Wf9
A656	38-11	IA453	
		R853	Oh07
B4	CK25		Oh7B
Ind461-3	W83	IA5125B	
		R825	R95
B37	CK26		Tx61M(A)
B37R	CK36	IL451B	
H93		Mo13	T8
	CK43	T101	Va35
B57	CMV3		
CK55		IL671A	T115
	CM105	P39(Robsn)	T139
B79	CM109		
CG8	CM113	Ind-B2	T220
Oh551	CM169	N28	T220A
R177			
	CO109	KP39	W22
C30	CO220	KP58K	W462
Ma20	CQ184		
P39(Crook.)		L289	W182B
	CQ178	MS153	W182BHt(B)
C123	CQ179	Os420	
EP1			W182BHt(A)
	CQ197	L317	WD
CG2	Oh43	Va58	
CG3			
	FL32	M14	
	IA2132	W705A	

#### ALLOZYME GENOTYPES OF WIDELY USED LINES

Allozyme genotypes for the most widely used publicly available lines are shown in table 8. These 39 lines were those used in 1980 as parents of hybrids for which more than 1 million pounds of seed were planted (Zuber and Darrah 1980). Fifty-one different alleles were found in these lines of the 80 identified in the entire set of lines assayed. Although this is 64% of the alleles present in the entire set of 406 lines, the entire set carries only 80/245 (33%) of the alleles that have been ascertained in corn and teosinte (table 3). So, although a large amount of variability is present

Table 9.—Allozyme genotypes of the 45 white corn lines of 406 U.S., Canadian, and European inbred lines of corn

LINE	Allele <sup>1</sup> at locus--															
	Acpl	Adhl	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5
A188	4	4	12	4.5	10	7	4	4	4	4	6	1	3.5	16	12	M
CI.64	3	4	9	4	6	7	4	4	4	4	6	6	6	16	12	M
CI.66	4	4	9	4	4	7	4	4	4	4	6	6	6	16	12	M
CI.127	4	4	9	5	6	2	4	4	4	4	4	6	3	16	12	M
GA209	2#	4	9	5	6	2	4	4	4	4	4	1	3	16	12	M
H21	4	4	12	4.5	4	2	4	4	4	4	6	6	3.5	16	12	M
H25	3	6	9	4.5	6	2	4	4	4	4	6	n	3	18	12	M
H30	2	4	9	4.5	6	7	4	4	4	4	4	6	3	16	12	M
K6	2	4	9	5	8	7	4	2	4	4	6	6	6	16	12	M
K41	2	4	12	5	n	7	4	4	4	4	6	6	3.5#	16	12	M
K55	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	M
K64	3	4	12	4.5	6	7	4	4	4	4	6	6	n	16	12	M
KY21	3	4	9	5	6	7	4	4	4	4	6	1	n	16	12	M
KY201	3	4	n	4	4	7	4	4	4	4	6	1	3	16	12	M
KY216	4	4	9	5	8	7	6	4	4	4	6	6	3.5	16	12	M
KY225	2*	4	9	4.5	6	6	4	4	4	4	6	6	6	16	12	M
KY226	3	4	9	5	6	6	6	4	4	6	4	6	3.5	16	12	M
KY228	2#	4	9	4.5	6	2	4	4	4	4	6	6	6	16	12	m
MICH37W	4	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	M
MO1W	2	6	9	5	6	6	6	4	4	4	4	6	3	16	12	M
MO14W	2	4	9	4.5	6	2	4	4	4	4	4	6	3	16	12	M
MO18W	2	6	9	4.5	6	6	4	4	4	4	4	6	3	16	12	M
MO20W	2	6	9	4.5	6	1	4	4	4	4	4	6	3	16	12	M
MO23W	4	4	9	4	10	2	4	4	4	4	6	6	3	16	12	M
MO24W	4	4	9	4	6	7#	4#	4	4	4	6	1	6	16	12	m
MO25W	4#	4	9	4.5	4	7#	4	2	4	4	4	1	3	16	12	M
MO505W	3	6	9	4	6	2	4	4	4	4	6	n	3	18	12	M
MO510W	3	4	9	4	6	7	6	4	4	4	6	6	3.5	16	12	M
MP305	4	4	9	4.5	n	6	4	4	4	4	4	1	6#	16	12	M
MP307	2	4	12	4	6	7	4	4	4	4	6	6	6	16	12	M
MP311	3	6	9	4.5	6	7	4	4	4	4	4	1	3	16	12	M
MP339	2	4	9	5	6	7	4	4	4	4	4	6	3	16	12	M
R95	4	4	9	4.5	6	7	4	4	4	4	4	1	3	16	12	M
SC359	3	4	9	4.5	6	1	4	4	4	4	4	1	3.5	16	12	M
T13	4	4	9	4.5	8	7	4	4	4	4	6	6	6	16	12	M

T61	2	4	9	5	6	7	4	4	4	4	4	4	6#	3	16	12	12	M	3.8	5	9	3	5
T101	4	4	9	4	6	6	4	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4
T111	2	4	9	4.5	4	6	4	4	4	4	4	4	6	6	16	12	12	M	2	5	9	4	4
T115	2	4	9	6	6	7	4	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	3	4
T139	2	4	9	6	6	7	4	4	4	4	4	4	1	3	16	12	12	M	3.8	5	9	3	4
TX61M(A)	4	4	9	4.5	6	7	4	4	4	4	4	4	1&	3	16	12	12	M	3.8	5	9	4	2
TX61M(B)	4	4	9	4.5	6	7	4	4	4	4	4	4	6&	3	16	12	12	M	3.8	5	9	4	2
TX585	3	4	9	5	6	2	4	4	4	4	6	6	6	6	16	12	12	M	2	5	9	4	4
33-16	2	4	9	5	4	7	4	4	4	4	4	6	6	3	16	12	12	M	2	5	9	4	5
4C082	3	4	9	4	6	7	4	4	4	4	4	6	10.5 n	n	16	12	12	M	3.8	5	9	3	5

The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

in the set of widely used lines, they have only about 21% (51/245) of the total number of alleles. Frequencies of alleles at individual loci in the set of widely used lines do not differ greatly from frequencies found in the entire set (table 4). Generally, alleles found rarely in the entire set are not found at all in the widely used set of 39 lines. There were thirty-six (92%) distinct allozyme genotypes found in the set of widely used lines (table 7). Thirty-three (85%) of these 39 lines are unique within the set, and 26 (67%) do not share their genotypes with any of the other lines in the entire set of 406 lines.

## ALLOZYME GENOTYPES OF WHITE CORN LINES

The 45 white corn lines assayed and their allozyme genotypes are presented in table 9. Forty-one (91%) of these lines are unique and form a slightly more variable group than the set of widely used, primarily yellow, lines (59 vs. 51 alleles, see tables 3 and 7). In this set of white lines, only two pairs of lines share the same allozyme genotype; T115 is identical to T139 and Tx61M(A) is identical to R95. Thirty-seven (82%) of these white lines do not share their genotypes with any of the other lines in the set of 406 lines. The white lines probably represent a wider geographic distribution than do the widely used lines listed in table 8. Also, relatively few of the white lines have actually been widely used. These facts may, at least partially, account for the greater variability noted in the set of white corn lines.

## ALLOZYME GENOTYPES OF SWEET CORN LINES

Allozyme genotypes for the 39 sweet corn lines assayed are shown in table 10. The amount of variability (51 alleles) is similar to that found in the widely used and white lines evaluated (table 3). Several alleles in the widely used and white line sets are not found in the sweet corn lines. But certain relatively rare alleles (particularly at the *Adh1*, *Cat3*, *Enp1*, and *Mdh1* loci) in the set of widely used lines have relatively high frequencies in the set of sweet corn lines (table 4). Twenty-six (67%) of the 39 sweet corn lines are unique (table 7). The other 13 lines share six different geno-



**Table 10.—Allozyme genotypes of the 39 sweet corn lines of 406 U.S., Canadian, and European inbred lines of corn**

LINE	Allele <sup>1</sup> at locus--																						
	Acpl	Adh1	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5	Mam	Pgd1	Pgd2	Pgal	Pgm2	Phil	
AA3	2	4	9	4.5#	6	7#	4	4	4	4	6	1	6	16	12	12	M	2	5	9	4	4	
AA8	2	4	12	4	6	2	4	4	4	4	6#	6	6	16	12	12	M	2	5	9	4	4	
C3	4	6	9	n	12	2	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4	
C13	4	6	9	6	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4	
C30	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4	
FL32	4	4	12	4	6	7	4	4	4	4	6	6	6	16	12	12	M	2	5	9	8	4	
FL56	4	4	9	4	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4	
IA453	4	4	9	4	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4	
IA2132	4	4	12	4	6	7	4	4	4	4	6	6	6	16	12	12	M	2	5	9	8	4	
IA2256	4	4	9	4	6	7	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4	
IA5125B	4	6	n	4.5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4	
IL11A	4	6	9	4	6	2.5	4	2	4	4	4	10.5	3	16	12	12	M	3.8	5	9	3#	4	
IL13B	4	4	9	4	6	7	4	4	4	4	4	10.5	6	16	12	15	M	3.8	5	9	3	4	
IL14H	4	n#	n	4	6	7	4	2	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4	
IL18B	4	6	9	4	10	7	4#	4	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4	
IL27A	3	6	9	4	10	7	4	4	4	4	4	10.5	6	16	12	12	M	3.8	5	9	8	4	
IL101T	4	6	n	4	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4	
IL110G	4	6	9	4	6	7	4	4	4	4	6	6	6#	16	12	12	M	3.8	5	9	4	4	
IL442A	4	4	12	4	6	1	4	2	4	4	6	10.5	6	16	12	12	M	2	5	9	4	4	
IL451B	4	4	9	4	6	6	4	4	4	4	4	6	6	16	12	12	M	3.8	5	9	4	4	
IL671A	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4	
IL677A	4	4	12	4.5	n	1	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	3	4	
IL685D	2	4	9	4.5	6	2	4	4	4	4	6	6	6	16	12	12	M	2	5	9	4	4	
IL731A	4	4	9	4.5	n	1	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	3	4	
MA20	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4	
MAC5NT	4	6	9	4	6	7	4	2	4	4	6	6	6	16	12	12	m	3.8	5	16	3	4	
ME2RT	4	6	9	4	6	7	4	4	4	4	4	10.5	6	16	12	12	M	3.8	5	9	4	4	
MEF156-55	4	6	9	4	6	6	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	3	4	
P39(ROBSN)	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4	
P39(CROOK)	4	4	9	4	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	4	4	
P51T	4	6	n	n	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	4	4	
P471-U6	3	6	12	4#	10	7#	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	3	4	
R825	4	6	n	4.5	6	7	4	4	4	4	6	6	6	16	12	12	M	3.8	5	9	8	4	
R839	4	4	9	6	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4	
R853	4	4	9	4	6	7	4	4	4	4	6	10.5	6	16	12	12	M	3.8	5	9	8	4	

S4	4	6	9	4	4	6	7	4	2	4	4	4	6	6	16	12	12	M	3.8	5	9	3	4
S8	4	6	9	4	4	6	7	4	2	4	4	4	6	6	16	12	12	M	3.8	5	9	8	4
81-1	2*	6	9	4	4	6	2	4	4	4	4	4	4	6	16	12	15	M	3.8	5	9	4	4
442	2	4	12	4#	4	6	7	4	2	4	4	4	6	6	16	12	12	M	2	5	9	4	4

<sup>1</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

types. Twenty-five (64%) of these sweet corn lines do not share their genotypes with any of the other lines in the entire set of lines assayed.

## ALLOZYME GENOTYPES OF POPCORN LINES

The 22 popcorn lines assayed and their allozyme genotypes are shown in table 11. Only 39 of the 80 inbred-line alleles are represented in the popcorn lines (table 3). Also, many of the lines are closely related as shown by the low number (13 or 59%) of unique lines (table 7). Nine of the popcorn lines share three allozyme genotypes. Many of the alleles in the widely used set of inbred lines are not found in the popcorn lines. But there are several alleles (particularly at the *Cat3*, *Enp1*, *Got1*, *Idh2*, *Mdh2*, and *Pgm2* loci) that are quite rare or not found in the widely used lines but that have relatively high frequencies in the popcorn lines. This indicates that the popcorn lines are somewhat distinct genetically from the widely used lines.

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Table 11.—Allozyme genotypes of the 22 popcorn lines of 406 U.S., Canadian, and European inbred lines of corn

LINE	Allele <sup>1</sup> at locus--															
	Acpl	Adh1	Cat3	E8	Enpl	Glul	Got1	Got2	Got3	Idh1	Idh2	Mdh1	Mdh2	Mdh3	Mdh4	Mdh5
A1-6	2L	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
C1-29(A)	4	4	9	4	8	7	6	4	4	4	6#	6	3&	16	12	12
C1-29(B)	4	4	9	4	8	7	6	4	4	4	6#	6	6&	16	12	12
C6-29(A)	4	4	n	4	8	7#	6	4	4	4	4#	6	6&	16	12	12
C6-29(B)	4	4	n	4	8	7#	6	4	4	4	4#	6	3&	16	12	12
H5505	3	6	n	4.5	8	7	6	4	4	4	4	6	6	16	12	12
HP62-49	2	4	n	4	6	7	4	4	4	4	4	6	6	16	12	12
HP301	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12
HP302	2	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
HP304W	2	4	9	4	6	6	6	4	4	4	6	6	3.5	16	12	12
I29	2	4	n	4.5	8	7	4	4	4	4	4	6	3.5	16	12	12
IDS28	2	4	n	4.5	6	n#	4	4	4	4	4	6	6	16	12	12
IDS69	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12
IDS91	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12
KP39	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12
KP58K	2	4	9	4	6	7	4	4	4	4	4	6	3.5	16	12	12
NYP501	3	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
SA24	2	4	9	4	6#	7	4	4	4	4	4	6#	3.5	16	12	12
SG16	2	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
SG18	2	4	9	4	6	7	4	4	4	4	4	6	6	16	12	12
SG1533	2	4	9	4.5	6	7	4	4	4	4	4	6	6	16	12	12
4722	4	4	12	4	6	6	4	4	4	4	4	6	3.5	16	12	12

<sup>1</sup>The numerical designations for the alleles are those used in our laboratory scoring. Alleles at a locus are numbered by their migration patterns. For the MDH loci, higher numbers correspond to greater anodal migration. For the other loci, higher numbers correspond to slower migration. At the Acpl locus, Acpl-2L and Acpl-2\* are variants of the Acpl-2 allele. The n symbolizes a recessive null allele. At the Mmm locus, the M refers to the dominant and the m to the recessive forms of the two commonly found alleles. For those lines having more than one allele at a locus, we have listed the most commonly found allele and followed the entry with #. For those lines having two equally frequent alleles at a locus, we listed the line twice (as A and B versions) and followed the entries for those alleles with &.

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